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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=8; day=19; hr=18; min=1; sec=22; ms=367; ]

=====

\*\*\*\*\*

Reviewer Comments:

<210> 25

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide for generation of TK mutants

<220>

<221> misc\_feature

<222> (1)...(51)

<223> n = A, T, C, or G

<400> 25

dactactgga tccatggcgg gccccaggcc tgtg

34

The above <222> response for 'N' locations for sequence id# 25 is invalid, there are only 34 nucleotides appearing in the sequence.

\*\*\*\*\*

Application No: 09173463 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2008-07-21 12:29:35.213  
**Finished:** 2008-07-21 12:29:39.388  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 175 ms  
**Total Warnings:** 168  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 172  
**Actual SeqID Count:** 172

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

**Input Set:**

**Output Set:**

**Started:** 2008-07-21 12:29:35.213  
**Finished:** 2008-07-21 12:29:39.388  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 175 ms  
**Total Warnings:** 168  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 172  
**Actual SeqID Count:** 172

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (47)
W 402	Undefined organism found in <213> in SEQ ID (59)
W 402	Undefined organism found in <213> in SEQ ID (60)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (105)
W 402	Undefined organism found in <213> in SEQ ID (134)

# SEQUENCE LISTING

<110> BLACK, Margaret E.

<120> THYMIDINE KINASE MUTANTS AND FUSION  
PROTEINS HAVING THYMIDINE KINASE AND GUANYLATE KINASE  
ACTIVITIES

<130> 60117-4

<140> 09173463

<141> 1998-10-14

<150> 60/061,812

<151> 1997-10-14

<160> 172

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1131

<212> DNA

<213> Herpesviridae sp.

<400> 1

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cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tctcgtctac 240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
atgacaagcg ccagataaac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggg tgggagctca catgccccgc cccgggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcggta ctttatgggc 540
agcatgacct ccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
accaacatcg tgcttggggc ccttcgggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct ggacctggct atgctggctg cgattcgccg cgtttacggg 720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggactgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc ccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatattacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttggaag tcttgcccaa acgcctccgt 960
tccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccc ggacgcctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg 1080
atatgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaactg a 1131
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<210> 2

<211> 52

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<223> Oligonucleotide for generation of TK mutants

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<210> 3

<211> 56

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide for generation of TK mutants

<220>

<221> misc\_feature

<222> (1)...(56)

<223> n = A, T, C, or G

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<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 4

cccctccagc gcggtac 17

<210> 5

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 5

cgcgctcgag gggagct 17

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

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<210> 7

<211> 11

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 7  
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<210> 8  
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<212> DNA  
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<220>  
<223> Oligonucleotides for generation of TK mutants

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<210> 9  
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<210> 11  
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<220>  
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<400> 11  
catgccttat gccgtga 17

<210> 12  
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<220>  
<221> CDS

<222> (1)...(33)

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1 5 10

<210> 13

<211> 11

<212> PRT

<213> Herpesviridae sp.

<400> 13

Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala  
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<210> 14

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> HSVTK Mutant

<220>

<221> CDS

<222> (1)...(33)

<400> 14

ccc atc gcc tcc ctc ctg tgc tac ccg gcc gcg 33  
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<210> 15

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> HSVTK Mutant

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<210> 16

<211> 33

<212> DNA

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<220>

<223> HSVTK Mutant

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Ser Ile Gly Ala Leu Gln Cys Tyr Pro Val Ala  
1 5 10

<210> 17  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> HSVTK Mutant

<400> 17  
Ser Ile Gly Ala Leu Gln Cys Tyr Pro Val Ala  
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<210> 18  
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<220>  
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<220>  
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<222> (1)...(33)

<400> 18  
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<220>  
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<400> 19  
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<210> 20  
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<213> Artificial Sequence

<220>

<223> HSVTK Mutant

<220>

<221> CDS

<222> (1)...(33)

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<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> HSVTK Mutant

<400> 21

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<211> 33

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<223> HSVTK Mutant

<220>

<221> CDS

<222> (1)...(33)

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<210> 23

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> HSVTK Mutant

<400> 23

Pro Ile Ala Ala Leu Val Cys Tyr Pro Ala Ala
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<210> 24  
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 <222> (1)...(58)  
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 <210> 25  
 <211> 34  
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 <220>  
 <221> misc\_feature  
 <222> (1)...(51)  
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 <210> 26  
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 <223> Primer  
  
 <400> 26  
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 <210> 27  
 <211> 33  
 <212> DNA  
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 <223> Primer  
  
 <400> 27  
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<211> 18	
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<400> 28	
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<211> 19	
<212> DNA	
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<223> Primer	
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<210> 30	
<211> 18	
<212> DNA	
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<223> Primer	
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<211> 18	
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<223> Primer	
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tgtaaaacga cggccagt	18
<210> 33	
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caggaaacag ctatgacc	18
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<211> 21	
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acctggataa agcctatg	18
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<211> 19	
<212> DNA	
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<223> Primer  
  
<400> 38  
aagcaggcgc tctctctga 19

<210> 39  
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<220>  
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<210> 40  
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<220>  
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<400> 40  
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<210> 41  
<211> 24  
<212> DNA  
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<210> 42  
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<210> 43  
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<400> 43  
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<210> 44  
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<220>  
<223> Primer

<400> 44  
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<210> 45  
<211> 42  
<212> DNA  
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<220>  
<223> Primer

<400> 45  
agtagtatcc atggagctgc cgcgcggcac caggccgctg ct 42

<210> 46  
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<212> PRT  
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<220>  
<223> Vector fusion peptide

<400> 46  
Met Ala Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15  
Arg Gly Ser Ser Met  
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<210> 47  
<211> 19  
<212> PRT  
<213> Herpesviridae sp.

<400> 47  
Ala Leu Thr Leu Ile Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys  
1 5 10 15  
Tyr Pro Ile

<210> 48  
<211> 606  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (7)...(597)

<400> 48

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ggatcc atg gcg ggc ccc agg cct gtg gtg ctg agc ggg cct tcg gga      48
      Met Ala Gly Pro Arg Pro Val Val Leu Ser Gly Pro Ser Gly
           1             5             10
```

```
gct ggg aag agc acc ctg ctg aag agg ctg ctc cag gag cac agc ggc      96
Ala Gly Lys Ser Thr Leu Leu Lys Arg Leu Leu Gln Glu His Ser Gly
      15             20             25             30
```

```
atc ttt ggc ttc agc gtg tcc cat acc acg agg aac ccg agg ccc ggc     144
Ile Phe Gly Phe Ser Val Ser His Thr Thr Arg Asn Pro Arg Pro Gly
           35             40             45
```

```
gag gag aac ggc aaa gat tac tac ttt gta acc agg gag gtg atg cag     192
Glu Glu Asn Gly Lys Asp Tyr Tyr Phe Val Thr Arg Glu Val Met Gln
           50             55             60
```

```
cgt gac ata gca gcc ggc gac ttc atc gag cat gcc gag ttc tcg ggg     240
Arg Asp Ile Ala Ala Gly Asp Phe Ile Glu His Ala Glu Phe Ser Gly
           65             70             75
```

```
aac ctg tat ggc acg agc aag gtg gcg gtg cag gcc gtg cag gcc atg     288
Asn Leu Tyr Gly Thr Ser Lys Val Ala Val Gln Ala Val Gln Ala Met
           80             85             90
```

```
aac cgc atc tgt gtg ctg gac gtg gac ctg cag ggt gtg cgg aac atc     336
Asn Arg Ile Cys Val Leu Asp Val Asp Leu Gln Gly Val Arg Asn Ile
           95             100            105            110
```

```
aag gcc acc gat ctg cgg ccc atc tac atc tct gtg cag ccg cct tca     384
Lys Ala Thr Asp Leu Arg Pro Ile Tyr Ile Ser Val Gln Pro Pro Ser
           115            120            125
```

```
ctg cac gtg ctg gag cag cgg ctg cgg cag cgc aac act gaa acc gag     432
Leu His Val Leu Glu Gln Arg Leu Arg Gln Arg Asn Thr Glu Thr Glu
           130            135            140
```

```
gag agc ctg gtg aag cgg ctg gct gct gcc cag gcc gac atg gag agc     480
Glu Ser Leu Val Lys Arg Leu Ala Ala Ala Gln Ala Asp Met Glu Ser
           145            150            155
```

```
agc aag gag ccc ggc ctg ttt gat gtg gtc atc att aac gac agc ctg     528
Ser Lys Glu Pro Gly Leu Phe Asp Val Val Ile Ile Asn Asp Ser Leu
           160            165            170
```

```
gac cag gcc tac gca gag ctg aag gag gcg ctc tct gag gaa atc aag     576
Asp Gln Ala Tyr Ala Glu Leu Lys Glu Ala Leu Ser Glu Glu Ile Lys
           175            180            185            190
```

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aaa gct caa agg acc ggc gcc tgaggatcc                                606
Lys Ala Gln Arg Thr Gly Ala
           195
```

<210> 49  
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 <212> PRT  
 <213> Homo sapiens

<400> 49  
 Met Ala Gly Pro Arg Pro Val Val Leu Ser Gly Pro Ser Gly Ala Gly  
 1 5 10 15  
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 20 25 30  
 Gly Phe Ser Val Ser His Thr Thr Arg Asn Pro Arg Pro Gly Glu Glu  
 35 40 45  
 Asn Gly Lys Asp Tyr Tyr Phe Val Thr Arg Glu Val Met Gln Arg Asp  
 50 55 60  
 Ile Ala Ala Gly Asp Phe Ile Glu His Ala Glu Phe Ser Gly Asn Leu  
 65 70 75 80  
 Tyr Gly Thr Ser Lys Val Ala Val Gln Ala Val Gln Ala Met Asn Arg  
 85 90 95  
 Ile Cys Val Leu Asp Val Asp Leu Gln Gly Val Arg Asn Ile Lys Ala  
 100 105 110  
 Thr Asp Leu Arg Pro Ile Tyr Ile Ser Val Gln Pro Pro Ser Leu His  
 115 120 125  
 Val Leu Glu Gln Arg Leu Arg Gln Arg Asn Thr Glu Thr Glu Glu Ser  
 130 135 140  
 Leu Val Lys Arg Leu Ala Ala Ala Gln Ala Asp Met Glu Ser Ser Lys  
 145 150 155 160  
 Glu Pro Gly Leu Phe Asp Val Val Ile Ile Asn Asp Ser Leu Asp Gln  
 165 170 175  
 Ala Tyr Ala Glu Leu Lys Glu Ala Leu Ser Glu Glu Ile Lys Lys Ala  
 180 185 190  
 Gln Arg Thr Gly Ala  
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<210> 50  
 <211> 660  
 <212> DNA  
 <213> Mus musculus

<220>  
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 <222> (25)...(618)

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 ctgggctcggg tccccgcgga cggc atg gca gga cct agg cca gta gtg ctg 51  
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 agc ggg ccg tca ggg gca ggg aag agc act ctg ctc aag aag ctg ttc 99  
 Ser Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Leu Lys Lys Leu Phe  
 10 15 20 25  
 cag gag cac agc agc atc ttc ggc ttc agt gtg tcc cat act aca agg 147  
 Gln Glu His Ser Ser Ile Phe Gly Phe Ser Val Ser His Thr Thr Arg  
 30 35 40



aac cca cga cct ggt gaa gaa gat ggc aaa gat tac tac ttt gtg acc	195
Asn Pro Arg Pro Gly Glu Glu Asp Gly Lys Asp Tyr Tyr Phe Val Thr	
45 50 55	
agg gag atg atg cag cgt gat att gca gca ggg gac ttc att gag cat	243
Arg Glu Met Met Met Gln Arg Asp Ile Ala Ala Gly Asp Phe Ile Glu His	
60 65 70	
gct gag ttc tca ggg aac ctg tac ggg aca agc aag gaa gct gtt cgg	291
Ala Glu Phe Ser Gly Asn Leu Tyr Gly Thr Ser Lys Glu Ala Val Arg	
75 80 85	
gct gtg cag gcc atg aac cgc atc tgc gtg cta gat gtc gac cta caa	339
Ala Val Gln Ala Met Asn Arg Ile Cys Val Leu Asp Val Asp Leu Gln	
90 95 100 105	
ggt gtg cgc agc atc aag aag act gat ctg tgt ccc atc tac atc ttt	387
Gly Val Arg Ser Ile Lys Lys Thr Asp Leu Cys Pro Ile Tyr Ile Phe	
110 115 120	
gtg cag cct ccc tcg ctg gac gtg ctg gag caa cga ctg cga ctg cgc	435
Val Gln Pro Pro Ser Leu Asp Val Leu Glu Gln Arg Leu Arg Leu Arg	
125 130 135	
aac act gag act gag gag agt ctg gca aag cgg ctg gca gct gca cgg	483
Asn Thr Glu Thr Glu Glu Ser Leu Ala Lys Arg Leu Ala Ala Ala Arg	
140 145 150	
aca gac atg gag agc agc aag gag cct ggc ttg ttt gac ctg gtg atc	531
Thr Asp Met Glu Ser Ser Lys Glu Pro Gly Leu Phe Asp Leu Val Ile	
155 160 165	
atc aat gac gac ctg gat aaa gcc tat gca acc ctg aag cag gcg ctc	579
Ile Asn Asp Asp Leu Asp L	